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Genetic and morphological trait structure in barley genotypes under rainfed conditions

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Abstract

Current research investigated twenty barley genotypes under rainfed conditions to examine variability in yield, its components, and morphological traits, while identifying key selection criteria. Biomass-related traits, such as biological yield and straw weight, displayed high variability, whereas thousand-seed weight showed minimal variation. Traits such as seed yield per plant, seed number per plant, and tiller number per plant exhibited moderate variability, highlighting their potential contribution to yield differences. Phenotypic correlation analysis revealed that yield was strongly linked to biomass yield and thousand-seed weight, suggesting that both source and sink components play essential roles in yield formation. Genotypic correlations were generally weaker than phenotypic correlations, reflecting the influence of environmental factors. However, thousand-seed weight, seed number per plant, and fertile tiller number consistently showed positive associations with yield, indicating their genetic stability and value for indirect selection. Factor analysis identified five independent factors. The first factor included biomass yield, straw weight, and seed yield, whereas the second factor represented seed yield per plant and seed number per plant. The third factor identified low-tillering genotypes, while the fourth factor reflected smaller seed size. Finally, the fifth factor captured variation in plant height. These factors emphasize the multifaceted nature of yield determination, with distinct separations between vegetative growth, reproductive efficiency, and plant size. Based on these findings, genetic improvement for seed yield under rainfed conditions should prioritize thousand-seed weight, seed number per plant, and fertile tiller number, while optimizing plant height.

Keywords: associations, biological yield, genetic correlation, seed properties

Introduction

Barley is used for animal feed and malt production, with limited use for human consumption. Its history of domestication and diverse genetic pool have enabled it to adapt to various conditions, ranging from cool temperate regions to warm subtropical and semi-arid areas (Jégo et al., 2024). In comparison to other cereals such as wheat, barley shows greater resilience to environmental stresses such

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as drought and salinity, making it a valuable crop in areas with limited water availability or unpredictable rainfall patterns (Poursafar et al., 2017; Alsamadany et al., 2024). As a result, barley is often cultivated in regions unsuitable for wheat production, including marginal lands where farming is economically challenging. In Iran, barley is the second most important cereal after wheat, grown on around 1.5 million hectares, with more than half of it cultivated under dryland farming systems (Ghahremaninejad et al., 2021). Crop productivity in these regions largely depends on the amount and distribution of seasonal rainfall. Winter barley typically performs better due to its efficient use of winter precipitation and extended growing season, while spring barley is preferred in regions where autumn sowing is not possible, at higher elevations, or where winter damage risks are higher (Akhavan & Saeidi, 2010; Saygili, 2023). Choosing between winter, spring, or facultative barley growth habits is thus a key factor in stabilizing production in variable climates. Rainfed agriculture is facing increasing pressures from climate change, including higher temperatures, altered precipitation patterns, and more extreme climate variability, particularly in semi-arid regions (Wang & Ren, 2025). These shifts have led to more frequent and intense weather events such as droughts, which threaten global cereal production, especially in dry and semi-dry regions. Facultative barley is emerging as a promising solution due to its high tolerance to cold temperatures, sensitivity to short-day photoperiods, and lack of a strict vernalization requirement, enabling flexible sowing in both autumn and spring (Muñoz-Amatrián et al., 2020). This adaptability allows farmers to adjust sowing dates based on unpredictable weather conditions, enhancing the resilience of barley-based cropping systems. Among the various environmental stresses, drought is a primary factor limiting barley yields. Water scarcity negatively impacts several morphological and physiological traits, including plant height, tiller number, spike length, spikelets per spike, and seed weight and number (Berki et al., 2025). The effect of drought varies depending on its timing, severity, and duration. Research shows that barley is relatively drought-tolerant during the early vegetative stages, particularly during tillering, but the reproductive phases including booting, flowering, and anthesis, are highly sensitive to water shortages (Sallam et al., 2019; Ahmad et al., 2022). Drought during the seed-filling stage further limits assimilate availability, reducing the duration of seed filling, resulting in smaller seeds and lower yields. In arid and semi-arid environments, drought often coincides with critical reproductive and seed-filling periods, leading to significant yield losses. A key strategy for drought adaptation is optimizing phenological development. By adjusting the timing and duration of growth stages, crops can complete sensitive stages before severe water deficits occur or minimize exposure during critical periods (Neupane et al., 2025). Effective barley breeding depends on the availability of genetic diversity for key agronomic traits and a thorough understanding of their inheritance and interactions. Seed yield is a complex trait influenced by various components such as the number of spikes per unit area, seeds per spike, and thousand-seed weight, each of which may respond differently to environmental stresses. Studies have indicated that barley seed yield has strong positive correlations with fertile tillers, seeds per spike, biomass production, and harvest index (Du et al., 2020), suggesting that genotypes with higher assimilate production and more efficient partitioning are more likely to produce higher yields. To improve barley yields under changing climate conditions, it is essential to understand the genetic variability and relationships between traits. Identifying the key traits that influence yield, particularly under rainfed conditions, will provide valuable insights for genetic improvement efforts and selection methods.

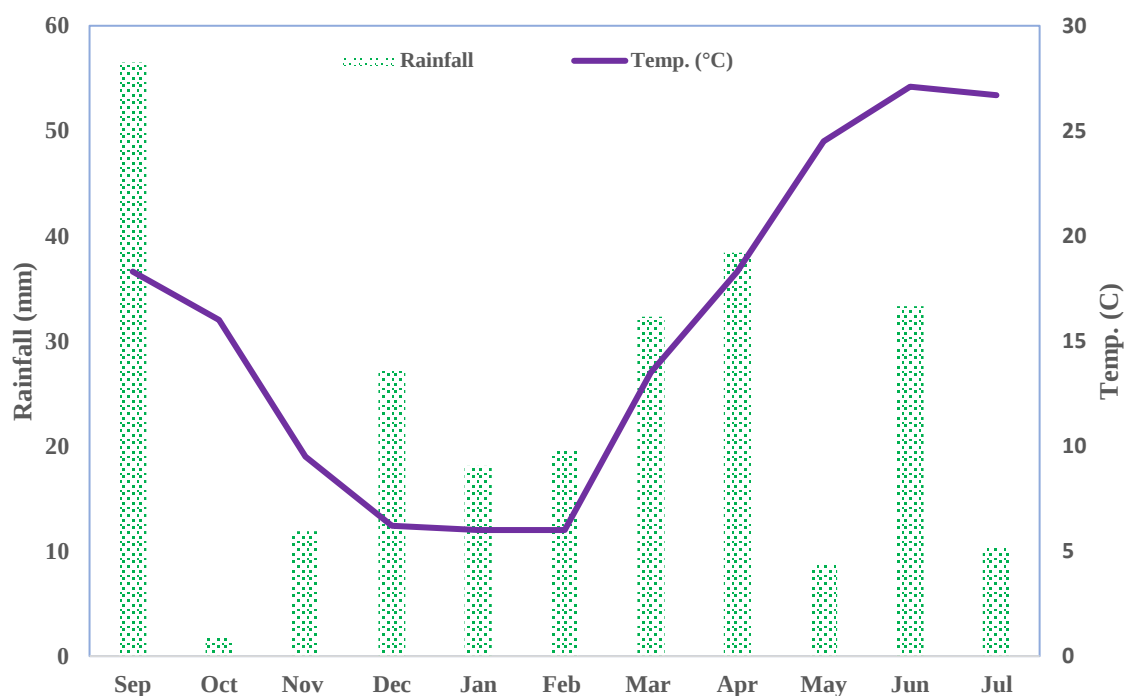


Fig. 1. The rainfall and temperature of experimental site.

Materials and Methods

The field trial was conducted at the Moghan region, northwestern Iran (39°38' N, 47°54' E), characterized by a semi-arid climate with warm summers, mild winters, and a relatively short cold period, according to the Köppen-Geiger climate classification. The long-term

mean annual temperature of the site is approximately 15 °C. The region receives about 335 mm of annual precipitation, mostly concentrated during winter and early spring (Fig. 1). The soil is classified as clay loam, with a neutral pH, an electrical conductivity of 2.4 dS m⁻¹, and low organic content, indicating moderately fertile conditions with slight salinity. Twenty barley genotypes, selected for their diverse morphological and agronomic characteristics (Table 1), were sourced from the SPII, Iran. The trial was set up in a randomized block design with three replicates under rainfed conditions, without irrigation. Prior to sowing, the experimental field was ploughed and disked to ensure a uniform seedbed. Sowing was carried out manually in the second week of November. Each plot consisted of six rows, three meters long, with 0.3 m spacing between rows and 0.1 m between plants. To minimize edge effects, data were collected only from plants in the central rows. Weed management was carried out using selective chlorophenoxy herbicides, supplemented with manual weeding as needed. Standard agronomic practices for barley cultivation in the region were consistently applied across all plots.

Table 1. Barley genotypes evaluated under rainfed conditions.

Code	Name or pedigree
G1	Mahour
G2	CBSS97M00850T-G-2M-1Y-2M-0Y
G3	CB06M00193T-C-9M-0AP-0AP-0AP
G4	CBSS07Y00696S-0AP-0AP
G5	CBSS05M00256S-2M-0Y-0M-0AP-0TR
G6	CBSS97M00850T-G-2M-1Y-2M-0TR
G7	CBSS06Y00079S-29Y-0M-0AP-0TR
G8	ICB86-0512-1AP-0TR-4AP-0TR-0AP
G9	ICB05-0498-5AP-0AP
G10	ICB05-0421-0AP-6AP-0AP
G11	ICB95-0204-0AP-16AP-0AP-4AP-0AP-9AP-0AP
G12	LBIRAN/UNA80//LIGNEE640/6/Vmorales
G13	CBSS05Y00158S- 25Y-0M-0Y-0M-4AP
G14	CBSW01WM00107T-0TOPY-6Y-1M-2Y-1M-0Y
G15	CBSS97M00850T-G-2M-1Y-2M-4AP
G16	ICB08-0124- OAP - OG-OG-OG- 5G
G17	CBSS05M00680D-K-2M-0M-0AP-0TR
G18	ICB09-1436-0AP-0TR-0AP-0TR-0AP-0TR
G19	TR145/195039
G20	M91178002/MAHIGAN

At physiological maturity, ten plants were randomly sampled from the central rows to measure several traits, including straw weight (SW), seed yield per plant (SYP), number of seeds per plant (NSP), tiller number (NT), fertile tiller number (NFT), spike length (SL), and plant height (PH). For biomass determination, all aboveground plant material from a specified central area in each plot was harvested and weighed to calculate biological yield (BY). Seed yield (SY) was measured after threshing and cleaning the samples, while thousand-seed weight (TSW) was determined by averaging the weight of three randomly selected samples of seeds per plot. Before conducting statistical analysis, the dataset was checked for normal distribution using the Shapiro-Wilk test, and the homogeneity of variances was verified with Levene's test based on plot means. Pearson's correlation coefficients were calculated to assess the strength and direction of phenotypic and genotypic relationships among the measured traits across genotypes, and the results were presented in a heatmap. The covariance matrix described additive variances (on the diagonal) and additive genetic covariances (off-diagonal). Factor analysis was performed using the correlation matrix to identify the most influential traits and to characterize the genotypes. Eigenvalues greater than 1.0 were retained according to Kaiser's criterion, and equamax rotation was applied to obtain more interpretable factor scores. All multivariate analyses were performed using Minitab 17.0. Communalities were computed to determine the proportion of variance in each trait explained by the extracted factors, thereby assessing the contribution of traits to the multivariate structure.

Results

Biomass-related traits showed greater variability, with biological yield (BY) and straw weight (SW) exhibiting high CV values of 24.5% and 31.6%, respectively, indicating significant differences in vegetative growth among genotypes. Among the yield components, seed yield per plant (SYP), number of seeds per plant (NSP), and number of tillers (NT) demonstrated moderate variability, highlighting their potential role in yield differentiation. In contrast, thousand-seed weight (TSW) showed relatively low variation (Table 2).



Morphological traits, including spike length (SL) and plant height (PH), exhibited low to moderate variability, with PH showing the lowest CV, suggesting that it is a more stable trait under the given conditions. The observed variation across yield, yield components, and morphological traits provided a strong foundation for correlation analysis to identify key determinants of seed yield in barley. A multi-season study on some barley landraces under rainfed conditions also reported significant trait variation, emphasizing the high variability in yield components typical of dryland barley (Elshafei et al., 2024).

Table 2. Descriptive statistical indices of barley traits.

Traits	Mean	CV	Variance	Median	Range
SY	2118.3	18.46	152985.4	2116.67	1313.33
BY	7567.2	24.54	3449581.1	7280.00	7331.78
SW	5448.9	31.61	2966205.3	5148.34	6021.78
SYP	1.79	14.13	0.06	1.82	0.92
NSP	55.2	14.27	62.04	54.17	32.00
TSW	32.46	8.46	7.54	32.82	8.91
NT	2.89	15.78	0.21	2.70	1.74
NFT	2.23	12.24	0.07	2.17	1.10
SL	5.88	10.11	0.35	5.85	2.53
PH	79.79	7.64	37.14	80.09	19.74

Traits are SY, seed yield; BY, biological yield; SW, straw weight; SYP, seed yield per plant; NSP, number of seeds per plant; TSW, thousand seed weight; NT, number of tillers; NFT, number of fertile tillers; SL, spike length; and PH, plant height.

The analysis of variance revealed significant genotype effects for most traits, with the main effect of genotype being significant for all traits except NSP and PH (Table 3).

Table 3. Analysis of variance for traits of barley genotypes.

Sources	DF	SY			BY		
		MS	F	P	MS	F	P
Block	2	68526.67	1.73	0.19	264736.71	0.32	0.72
Treatment	19	458956.14	11.59	0.00	10348741.52	12.69	0.00
Residuals	38	39600.35			815367.59		
Sources	DF	SW			SYP		
		MS	F	P	MS	F	P
Block	2	72485.78	0.11	0.89	0.45	3.20	0.05
Treatment	19	8898613.15	14.09	0.00	0.19	1.35	0.21
Residuals	38	631494.05			0.14		
Sources	DF	NSP			TSW		
		MS	F	P	MS	F	P
Block	2	163.80	1.29	0.29	61.38	9.43	0.00
Treatment	19	186.15	1.47	0.15	22.63	3.48	0.00
Residuals	38	126.61			6.51		
Sources	DF	NFT			NT		
		MS	F	P	MS	F	P
Block	2	0.04	0.14	0.87	0.59	5.39	0.01
Treatment	19	0.62	2.34	0.01	0.22	2.04	0.03
Residuals	38	0.26			0.11		
Sources	DF	SL			PH		
		MS	F	P	MS	F	P
Block	2	0.07	0.23	0.79	6937.64	31.63	0.00
Treatment	19	1.06	3.64	0.00	290.78	1.33	0.22
Residuals	38	0.29			219.37		

Traits are SY, seed yield; BY, biological yield; SW, straw weight; SYP, seed yield per plant; NSP, number of seeds per plant; TSW, thousand seed weight; NT, number of tillers; NFT, number of fertile tillers; SL, spike length; and PH, plant height.

The final yield performance (SY) was positively associated with biomass yield and thousand-seed weight (Fig. 2), suggesting that both biomass production and seed size are important determinants of yield. A strong and significant correlation was observed between BY and SW, reflecting their close biological relationship. BY was also positively correlated with plant height (Fig. 2), indicating that taller plants tended to accumulate greater biomass. Among yield components, SYP showed a strong positive correlation with NSP, emphasizing NSP as a major determinant of seed yield per plant. Additionally, fertile tiller number (NFT) was positively correlated with NT, suggesting that tiller fertility largely depends on tiller production capacity. However, SY was negatively correlated with both spike length and plant height, implying that taller plants or longer spikes did not necessarily translate into higher seed yield. TSW also showed a significant negative correlation with SL, suggesting a trade-off between spike elongation and seed weight (Fig. 2). These correlations illustrate how environmental variation under rainfed conditions can strongly affect phenotypic relationships, highlighting the importance of both phenotypic and genotypic correlations in breeding strategies. The Pearson correlation coefficients revealed that TSW, BY, and fertility-related traits (NFT, NSP) were more strongly associated with seed yield than plant height or spike length. These relationships provide a solid foundation for future breeding efforts. A study on spring malting barley identified seed number and spike number per unit area as the main yield components, while thousand-seed weight was less variable and poorly correlated with yield, underscoring the dominant role of reproductive components in yield variation (Hu et al., 2021). This finding aligns with the importance of NSP and SYP observed in the current study. Similarly, research on barley genotypes under rainfed conditions demonstrated that seed yield and its components are influenced by environmental interactions, with traits like plant height and kernel weight varying widely among genotypes in dryland conditions (Roohi et al., 2022). This supports the current finding of considerable variability and the role of environmental factors in shaping phenotypic correlations. Multivariate analyses of barley landraces have also shown that the number of spikes and seeds per spike are closely associated with seed yield (Derbew, 2020), which echoes the positive correlations between SYP and NSP found in the current dataset and underscores the role of reproductive traits in determining final yield. Therefore, traits such as biomass yield, seeds per plant, and thousand-seed weight are key contributors to seed yield, while plant height and spike length may have weaker or context-dependent associations.

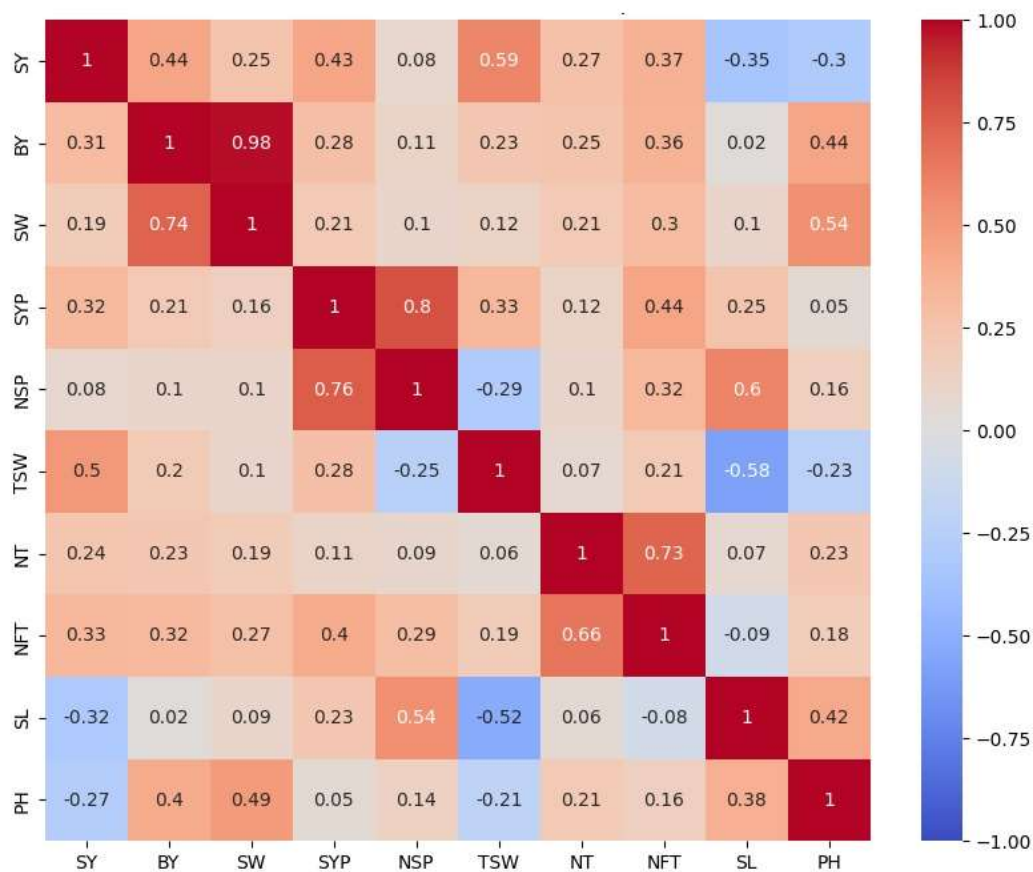


Fig. 2. Heatmap of Pearson correlations (down diagonal) and genotypic correlations (up diagonal) for barley traits. Critical values $P < 0.05$ and $P < 0.01$ (with 18 degrees of freedom) are 0.44 and 0.56, respectively.

Seed yield (SY) displayed positive genotypic correlations with thousand-seed weight (TSW) (Fig. 2), further supporting TSW as a genetically regulated and key contributor to yield. A significant genotypic correlation was also observed between biomass yield (BY) and straw weight (SW), confirming that straw production is a major genetically determined component of overall biomass. Among the yield components, seed yield per plant (SYP) was strongly and significantly correlated with the number of seeds per plant (NSP),

highlighting NSP as the primary genetic determinant of yield per plant. Additionally, the number of tillers (NT) was strongly positively correlated with the number of fertile tillers (NFT) (Fig. 2), indicating that tiller fertility is largely under genetic control. Negative genetic associations were observed between TSW and spike length (SL), suggesting a genetic trade-off between seed size and spike length. Similarly, a negative correlation between TSW and NSP hinted at a genetic compensation between seed number and seed weight. The lower genotypic correlations compared to phenotypic correlations are biologically reasonable, reflecting the influence of environmental variance on trait relationships. When two traits respond similarly to environmental conditions like moisture availability, the environmental variance can inflate phenotypic correlations (Walter et al., 2024). In this study, traits linked to biomass accumulation and yield responded in a coordinated manner to favorable environmental conditions, which resulted in stronger phenotypic correlations. However, when environmental effects were accounted for, the genetic associations among these traits became weaker, leading to lower genotypic correlations (Sabaghnia et al., 2024). This suggests that part of the phenotypic relationship is shaped by environmental factors rather than being solely genetically determined. Strong phenotypic correlations, such as those between biomass yield and spike length or seed yield per plant and number of seeds per plant, remained high genotypically but were somewhat reduced, indicating that these associations are partly genetic but also reinforced by environmental factors. For seed yield, phenotypic correlations with TSW and BY were stronger than genotypic correlations, suggesting that environmental factors contribute significantly to seed filling and biomass production. Negative correlations with plant height and spike length were consistent at both phenotypic and genotypic levels, but were weaker genetically, indicating that these traits are less closely related to yield at the genetic level. Therefore, relying solely on phenotypic correlations for selection could be misleading, particularly under variable environmental conditions (Arnold et al., 2019). Traits that exhibit consistent and moderate correlations at both phenotypic and genotypic levels (such as TSW, NSP, and NFT) are more reliable as indirect selection criteria. The Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (0.627) and Bartlett's test of sphericity (60.88) confirmed the appropriateness of factor analysis for the dataset. Five factors were extracted, each with eigenvalues greater than 1.0, together accounting for 85% of the phenotypic variation. This suggests that the traits were well represented by a limited number of underlying latent factors (Table 4). Eigenvectors show the underlying covariance structure of the dataset by grouping traits that vary together across genotypes. Traits with high loadings on the same eigenvector are highly correlated and controlled by similar physiological or developmental processes. The eigenvalue (λ) associated with each eigenvector expresses the amount of variance captured by that axis. In the current study, the first few eigenvectors captured the majority of variation, indicating that complex trait interactions can be effectively summarized by a limited number of latent dimensions. Thus, eigenvectors simplify high-dimensional trait data into biologically interpretable components, allowing clearer identification of key trait complexes governing yield formation and plant architecture. The first factor (F1) accounted for 23% of the variation and was characterized by positive scores for biomass yield, straw weight, and seed yield, thus labeled as the yield potential factor. This factor reflects plant productivity and biomass accumulation, emphasizing the role of assimilate production in determining seed yield.

Table 4. Equamax rotation of the obtained scores of factor analysis of traits in barley genotypes.

Traits	F-1	F-2	F-3	F-4	F-5	Comm.†
SY	0.68	0.17	-0.18	-0.30	0.22	0.88
BY	0.81	0.09	-0.12	-0.10	-0.10	0.99
SW	0.83	0.06	-0.10	-0.03	-0.18	0.98
SYP	0.12	0.87	-0.09	-0.29	0.00	0.99
NSP	0.04	0.88	-0.08	0.27	-0.04	0.97
TSW	0.10	0.01	-0.05	-0.88	0.09	0.94
NT	0.10	0.02	-0.93	-0.02	-0.08	0.92
NFT	0.18	0.21	-0.74	-0.08	-0.05	0.88
SL	0.03	0.33	0.01	0.24	-0.20	0.83
PH	0.35	0.04	-0.12	0.10	-0.83	0.92
λ	2.02	1.89	1.58	1.22	1.02	
%	0.23	0.21	0.18	0.14	0.09	

†Communalities Traits are SY, seed yield; BY, biological yield; SW, straw weight; SYP, seed yield per plant; NSP, number of seeds per plant; TSW, thousand seed weight; NT, number of tillers; NFT, number of fertile tillers; SL, spike length; and PH, plant height.

The second factor (F2), which explained 21% of the variance, showed positive loadings for seed yield per plant and number of seeds per plant, with a moderate contribution from spike length, and was designated the seed capacity factor (Table 4). This factor represented reproductive efficiency, particularly the genetic regulation of seed number, as further supported by the strong phenotypic and genotypic correlations between SYP and NSP (Fig. 2). The third factor (F3), which explained 18% of the variation, was defined by negative loadings for total tillers and fertile tillers, making it the low-tillering factor, while the fourth factor (F4), which accounted for 14% of the variance, was dominated by a negative loading for thousand-seed weight, labeling it the seed-size reduction factor, indicating smaller seed size (Table 4). The fifth factor (F5), which explained 9% of the variability, showed a negative loading for plant height,

marking it the "dwarfism factor," suggesting that plant height operates independently from most yield and yield-component traits. The high communalities for all traits indicated that the extracted factors sufficiently explained the observed variation, validating the use of factor analysis for dimensionality reduction in current research. The current factor analysis structure corroborated the results of the phenotypic and genotypic correlation analyses, as highly correlated traits clustered within the same factors, while traits with weaker or negative correlations to seed yield were grouped into separate factors. This separation suggests that seed yield in barley is governed by multiple, relatively independent biological processes, including yield potential, seed capacity, low-tillering, seed-size reduction factor, and dwarfism traits. From a breeding perspective, F1 (yield potential) and F2 (seed capacity) were the most influential factors for improving yield, while F4 (seed-size reduction factor) offered an additional independent selection axis. Simultaneous selection for traits representing these factors could more effectively enhance seed yield than selecting based solely on plant height or spike length. Principal component analysis of Egyptian barley landraces (Abdelghany et al., 2025) revealed that the first two components accounted for much of the variation, and seed yield and its components clustered into major groups, supporting the notion that a small number of trait dimensions capture the bulk of diversity in barley agronomic performance. Traits such as spike number and seeds per spike contributed significantly to yield, reinforcing the importance of reproductive traits in yield formation, and aligning with the biological interpretation of factors F1 and F2 in the current study (Roohi et al., 2022). Similarly, plant height and other structural traits often formed separate axes from yield and reproductive traits, suggesting that plant stature and yield potential can be genetically and environmentally independent (Wang et al., 2022). Therefore, complex traits in barley can be effectively summarized by a few latent factors, with high-impact yield components like seed number, biomass, and seed weight tending to group into interpretable indices. Similar to the current results, previous studies have also shown that multiple factors explain major sources of variation, including yield potential, seed capacity, and tillering in barley. Past studies also found multiple underlying components structuring trait variation. For example, principal component analysis of barley genotypes showed that five factors explained about 73% of the variation, with the first factor associated with yield and component traits such as plant dry weight, seed weight per plant, straw weight, and fertile tiller number (Kumar et al., 2024), consistent with current yield and biomass-related factor. Also, some previous barley studies observed that traits like straw weight, biological yield, and grain yield tend to cluster together or load on the same component axis (Hansson et al., 2024), indicating they contribute jointly to overall productivity, similar to the positive scores for SY, BY and SW in the identified first factor. Thus, seed yield of barley and its components are controlled by multiple genetic factors with both additive and non-additive contributions, and this phenomenon underpins why separate statistical factors emerge for traits like yield potential, reproductive efficiency, and morphological features in current work.

Discussion

The present study demonstrated both phenotypic and genotypic variation among barley genotypes evaluated under rainfed conditions, showcasing the ability of barley to express a range of adaptive responses under natural moisture limitations. Rainfed environments impose variable and often severe drought stress, which significantly impacts the expression of yield-related traits (Sabaghnia et al., 2023). The observed variability reflected not only genetic differences but also genotype-specific drought adaptation mechanisms. Phenotypic correlations revealed positive associations between seed yield, biomass yield, and thousand-seed weight, suggesting that in rainfed environments, the ability to sustain biomass production and seed filling despite limited water availability is crucial for yield formation. Similar results have been found in dryland barley, where genotypes that can maintain assimilate production during post-anthesis drought conditions tend to achieve higher seed yields (Sallam et al., 2019; Mahalingam et al., 2022). The positive relationship between biomass yield and straw weight further indicated that genotypes with vigorous early vegetative growth are better equipped to capture and utilize the limited soil moisture available. The weak or negative associations between seed yield and plant height or spike length are particularly relevant in rainfed conditions. Taller plants generally have higher transpiration demands and are more vulnerable to terminal drought, which can limit seed filling. Previous studies on rainfed barley have indicated that moderate plant height is beneficial, as it balances biomass production with reduced water loss, ultimately improving the harvest index (Goñi et al., 2021; Kim et al., 2022). The negative genotypic correlations observed in this study suggest that shorter or moderately tall genotypes have a genetic advantage under moisture-limited environments. Genotypic correlations were generally lower than phenotypic correlations, indicating that environmental variance in rainfed conditions inflated phenotypic relationships among traits. In such environments, episodic rainfall events can simultaneously enhance multiple traits such as biomass, seed number, and seed weight, resulting in strong phenotypic associations that may not be fully genetically controlled (Hunt et al., 2021). This phenomenon is well-documented in dryland barley, emphasizing the importance of conducting genotypic analysis when identifying reliable selection criteria for drought-prone environments. The correlation between seed yield per plant and number of seeds per plant at both phenotypic and genotypic levels underscored seed number as a primary determinant of yield stability under rainfed conditions. Seed number is often determined earlier in the crop cycle compared to seed weight, making it a more dependable trait for selection under drought stress. Also, the strong genetic relationship between total tillers and fertile tillers emphasized the critical role of tiller survival under moisture stress, as drought frequently induces tiller abortion in barley (Zhang et al., 2025). Factor analysis further illuminated the structure of trait relationships under rainfed conditions, where traits associated with biomass accumulation and yield clustered together. This suggests that source strength, specifically the ability to maintain biomass production, is a key driver of yield even in water-limited environments. Seed yield per plant and seeds per plant were grouped into a distinct factor related to reproductive efficiency, while thousand-seed weight loaded independently. This independent loading suggests that seed filling capacity under drought is controlled by partially distinct genetic mechanisms. Plant height, on the other hand, formed a separate factor, reinforcing its limited utility as a direct selection trait for yield in rainfed environments. By combining correlation and factor analyses, the study concluded that seed yield under rainfed conditions is regulated by multiple adaptive components, including biomass maintenance, seed number, tiller fertility, and seed filling efficiency. From a breeding perspective, the results suggest that selection under rainfed conditions should prioritize traits like thousand-seed weight, seeds per plant, and fertile tillers, as these traits exhibit strong genetic associations with seed yield and are less sensitive to

environmental variability. While plant height remains agronomically important, it should be optimized for drought adaptation rather than being the primary criterion for yield selection.

Conclusions

The research showed significant phenotypic and genotypic variation among barley genotypes under rainfed conditions, highlighting the ability of barley to adapt to such environments. Seed yield was most closely related to biomass production, seed number per plant, and thousand-seed weight, while plant height and spike length had weaker or context-dependent effects. Phenotypic correlations were generally stronger than genotypic correlations, suggesting that environmental factors played a significant role in trait expression. Factor analysis identified five distinct trait dimensions: yield potential, seed capacity, low-tillering, seed-size reduction factor, and dwarfism, which helped clarify the underlying structure of yield determinants.

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